

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/564,369  
Source: IFWP  
Date Processed by STIC: 1-23-06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 01/23/2006

PATENT APPLICATION: US/10/564,369

TIME: 09:55:55

Input Set : A:\sequence listing.txt

Output Set: N:\CRF4\01232006\J564369.raw

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3 <110> APPLICANT: Oregon Health & Science University
4   Moses, Ashlee
5   Nelson, Jay
6   Fruh, Klaus
7   King, Jeff
8   Jelinek, Laura
9   Hirsch, Alec
10  DeFilippis, Victor
12 <120> TITLE OF INVENTION: METHODS OF TREATMENT AND DIAGNOSIS USING
MODULATORS OF
13   VIRUS-INDUCED CELLULAR GENE SEQUENCES
15 <130> FILE REFERENCE: 899-73077-04
C--> 17 <140> CURRENT APPLICATION NUMBER: US/10/564,369
C--> 18 <141> CURRENT FILING DATE: 2006-01-11
20 <150> PRIOR APPLICATION NUMBER: PCT/US2004/011988
21 <151> PRIOR FILING DATE: 2004-04-15
23 <150> PRIOR APPLICATION NUMBER: US 60/486,694
24 <151> PRIOR FILING DATE: 2003-07-11
26 <150> PRIOR APPLICATION NUMBER: US 60/533,103
27 <151> PRIOR FILING DATE: 2003-12-29
29 <160> NUMBER OF SEQ ID NOS: 17
31 <170> SOFTWARE: PatentIn version 3.2
33 <210> SEQ ID NO: 1
34 <211> LENGTH: 1232
35 <212> TYPE: DNA
36 <213> ORGANISM: Homo sapiens
39 <220> FEATURE:
40 <221> NAME/KEY: CDS
41 <222> LOCATION: (19)..(1044)
43 <400> SEQUENCE: 1
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45           Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro
46           1           5           10
48 acg gaa aag cag cgg tac ctg gat gag gcc gag aga gag aag cag cag      99
49 Thr Glu Lys Gln Arg Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln
50           15           20           25
52 tac atg aag gag ctg cgg gcg tac cag cag tct gaa gcc tat aag atg      147
53 Tyr Met Lys Glu Leu Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met
54           30           35           40
56 tgc acg gag aag atc cag gag aag aag atc aag aaa gaa gac tcg agc      195
57 Cys Thr Glu Lys Ile Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser
58           45           50           55
60 tct ggg ctc atg aac act ctc ctg aat gga cac aag ggt ggg gac tgc      243
61 Ser Gly Leu Met Asn Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys

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62	60					65				70				75					
64	gat	ggc	ttc	tcc	acc	ttc	gat	gtt	ccc	atc	ttc	act	gaa	gag	ttc	ttg			291
65	Asp	Gly	Phe	Ser	Thr	Phe	Asp	Val	Pro	Ile	Phe	Thr	Glu	Glu	Phe	Leu			
66						80				85				90					
68	gac	caa	aac	aaa	gcg	cgt	gag	gcg	gag	ctt	cgg	cgc	ttg	cgg	aag	atg			339
69	Asp	Gln	Asn	Lys	Ala	Arg	Glu	Ala	Glu	Leu	Arg	Arg	Leu	Arg	Lys	Met			
70				95					100				105						
72	aat	gtg	gcc	ttc	gag	gag	cag	aac	gcg	gta	ctg	cag	agg	caa	aac	gca			387
73	Asn	Val	Ala	Phe	Glu	Glu	Gln	Asn	Ala	Val	Leu	Gln	Arg	Gln	Asn	Ala			
74			110					115				120							
76	gag	cat	gag	cag	cgc	gcg	cga	gcg	tct	gga	gca	gga	gct	ggc	gct	gga			435
77	Glu	His	Glu	Gln	Arg	Ala	Arg	Ala	Ser	Gly	Ala	Gly	Ala	Gly	Ala	Gly			
78		125					130					135							
80	gga	gcg	gag	gac	gct	ggc	gct	gca	gca	gca	gct	cca	ggc	cgt	gcg	cca			483
81	Gly	Ala	Glu	Asp	Ala	Gly	Ala	Ala	Ala	Ala	Ala	Pro	Gly	Arg	Ala	Pro			
82	140					145				150				155					
84	ggc	gct	cac	cgc	cag	ctt	cgc	ctc	act	gcc	ggg	gcc	ggg	cac	ggg	cga			531
85	Gly	Ala	His	Arg	Gln	Leu	Arg	Leu	Thr	Ala	Gly	Ala	Gly	His	Gly	Arg			
86				160				165				170							
88	aac	gcc	cac	gct	ggg	cac	tct	gga	ctt	cta	cat	ggc	ccg	gct	tca	cgg			579
89	Asn	Ala	His	Ala	Gly	His	Ser	Gly	Leu	Leu	His	Gly	Pro	Ala	Ser	Arg			
90			175					180				185							
92	agc	cat	cga	gcg	cga	ccc	cgc	cca	gca	cga	gaa	gct	cat	cgt	ccg	cat			627
93	Ser	His	Arg	Ala	Arg	Pro	Arg	Pro	Ala	Arg	Glu	Ala	His	Arg	Pro	His			
94			190					195				200							
96	caa	gga	aat	cct	ggc	cca	ggg	cgc	cag	cga	gca	cct	gtg	agg	agt	ggg			675
97	Gln	Gly	Asn	Pro	Gly	Pro	Gly	Arg	Gln	Arg	Ala	Pro	Val	Arg	Ser	Gly			
98		205				210				215									
100	cgg	gcc	cac	gat	gca	gag	gag	aag	ctg	tgg	gcg	cgg	ccc	tgc	cac	acc			723
101	Arg	Ala	His	Asp	Ala	Glu	Lys	Leu	Trp	Ala	Arg	Pro	Cys	His	Thr				
102	220					225				230			235						
104	cca	ccc	cgt	gga	cga	gag	gct	ggg	ggg	cca	ccc	ttt	ggg	gcc	tgg	tcc			771
105	Pro	Pro	Arg	Gly	Arg	Glu	Ala	Gly	Gly	Pro	Pro	Phe	Gly	Ala	Trp	Ser			
106				240				245				250							
108	cat	cct	gca	cct	ttg	ggg	gct	cca	gcc	ccc	cta	aaa	tta	aat	ttc	tgc			819
109	His	Pro	Ala	Pro	Leu	Gly	Ala	Pro	Ala	Pro	Leu	Lys	Leu	Asn	Phe	Cys			
110			255					260				265							
112	agc	atc	cct	tta	gct	ttc	aat	ctc	ccc	agc	ccc	ctg	aac	ccg	gaa	aaa			867
113	Ser	Ile	Pro	Leu	Ala	Phe	Asn	Leu	Pro	Ser	Pro	Leu	Asn	Pro	Glu	Lys			
114			270					275				280							
116	gca	ctc	gct	gcg	cga	tac	acc	cag	aag	aac	ctc	aca	gcc	gag	ggg	gcc			915
117	Ala	Leu	Ala	Ala	Arg	Tyr	Thr	Gln	Lys	Asn	Leu	Thr	Ala	Glu	Gly	Ala			
118		285				290				295									
120	cct	cct	cgg	agg	aca	gcc	acg	cgc	tac	act	ggc	tct	ccg	ggc	cac	ccc			963
121	Pro	Pro	Arg	Arg	Thr	Ala	Thr	Arg	Tyr	Thr	Gly	Ser	Pro	Gly	His	Pro			
122	300					305				310			315						
124	cag	gac	aca	ggg	cag	acg	aaa	ccc	acc	ccc	agc	aca	cgg	cag	gac	ccc			1011
125	Gln	Asp	Thr	Gly	Gln	Thr	Lys	Pro	Thr	Pro	Ser	Thr	Arg	Gln	Asp	Pro			
126				320				325				330							

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128 cca aat tac tca cta cgg ggg gct gtg cca tag gccacacagg aagctgcctt      1064
129 Pro Asn Tyr Ser Leu Arg Gly Ala Val Pro
130          335          340
132 gtggggactt acctggggtg tccccgcacat gcctgtaccc cagatgggtg ggggccggct      1124
134 ttgcccatcc tgctctcctc cagccgaggg accctgggtg ggggtggctcc ttctcactgc      1184
136 tggatccgga ctttttaaataaaaaacaagt aaaatttgtg ttttaaaa      1232
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 341
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
146 Met Leu Gly Ala Glu Trp Ser Lys Leu Gln Pro Thr Glu Lys Gln Arg
147 1          5          10          15
150 Tyr Leu Asp Glu Ala Glu Arg Glu Lys Gln Gln Tyr Met Lys Glu Leu
151          20          25          30
154 Arg Ala Tyr Gln Gln Ser Glu Ala Tyr Lys Met Cys Thr Glu Lys Ile
155          35          40          45
158 Gln Glu Lys Lys Ile Lys Lys Glu Asp Ser Ser Ser Gly Leu Met Asn
159          50          55          60
162 Thr Leu Leu Asn Gly His Lys Gly Gly Asp Cys Asp Gly Phe Ser Thr
163 65          70          75          80
166 Phe Asp Val Pro Ile Phe Thr Glu Glu Phe Leu Asp Gln Asn Lys Ala
167          85          90          95
170 Arg Glu Ala Glu Leu Arg Arg Leu Arg Lys Met Asn Val Ala Phe Glu
171          100          105          110
174 Glu Gln Asn Ala Val Leu Gln Arg Gln Asn Ala Glu His Glu Gln Arg
175          115          120          125
178 Ala Arg Ala Ser Gly Ala Gly Ala Gly Ala Gly Gly Ala Glu Asp Ala
179          130          135          140
182 Gly Ala Ala Ala Ala Ala Pro Gly Arg Ala Pro Gly Ala His Arg Gln
183 145          150          155          160
186 Leu Arg Leu Thr Ala Gly Ala Gly His Gly Arg Asn Ala His Ala Gly
187          165          170          175
190 His Ser Gly Leu Leu His Gly Pro Ala Ser Arg Ser His Arg Ala Arg
191          180          185          190
194 Pro Arg Pro Ala Arg Glu Ala His Arg Pro His Gln Gly Asn Pro Gly
195          195          200          205
198 Pro Gly Arg Gln Arg Ala Pro Val Arg Ser Gly Arg Ala His Asp Ala
199          210          215          220
202 Glu Glu Lys Leu Trp Ala Arg Pro Cys His Thr Pro Pro Arg Gly Arg
203 225          230          235          240
206 Glu Ala Gly Gly Pro Pro Phe Gly Ala Trp Ser His Pro Ala Pro Leu
207          245          250          255
210 Gly Ala Pro Ala Pro Leu Lys Leu Asn Phe Cys Ser Ile Pro Leu Ala
211          260          265          270
214 Phe Asn Leu Pro Ser Pro Leu Asn Pro Glu Lys Ala Leu Ala Ala Arg
215          275          280          285
218 Tyr Thr Gln Lys Asn Leu Thr Ala Glu Gly Ala Pro Pro Arg Arg Thr
219          290          295          300

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222 Ala Thr Arg Tyr Thr Gly Ser Pro Gly His Pro Gln Asp Thr Gly Gln
223 305                               310                               315                               320
226 Thr Lys Pro Thr Pro Ser Thr Arg Gln Asp Pro Pro Asn Tyr Ser Leu
227                               325                               330                               335
230 Arg Gly Ala Val Pro
231                               340
234 <210> SEQ ID NO: 3
235 <211> LENGTH: 3870
236 <212> TYPE: DNA
237 <213> ORGANISM: Homo sapiens
240 <220> FEATURE:
241 <221> NAME/KEY: CDS
242 <222> LOCATION: (179)..(1642)
244 <400> SEQUENCE: 3
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247 aaaagttttt cttgtggaac aagttaacac tagatggcag ataacagact gaggagtgag      120
249 ctgcttctga ctcgattaaa aagggagtga gccataactg gcggctgctc ttctgccca      178
251 atg agc ctc ccc aat tcc tcc tgc ctc tta gaa gac aag atg tgt gag      226
252 Met Ser Leu Pro Asn Ser Ser Cys Leu Leu Glu Asp Lys Met Cys Glu
253 1                               5                               10                               15
255 ggc aac aag acc act atg gcc agc ccc cag ctg atg ccc ctg gtg gtg      274
256 Gly Asn Lys Thr Thr Met Ala Ser Pro Gln Leu Met Pro Leu Val Val
257                               20                               25                               30
259 gtc ctg agc act atc tgc ttg gtc aca gta ggg ctc aac ctg ctg gtg      322
260 Val Leu Ser Thr Ile Cys Leu Val Thr Val Gly Leu Asn Leu Leu Val
261                               35                               40                               45
263 ctg tat gcc gta cgg agt gag cgg aag ctc cac act gtg ggg aac ctg      370
264 Leu Tyr Ala Val Arg Ser Glu Arg Lys Leu His Thr Val Gly Asn Leu
265                               50                               55                               60
267 tac atc gtc agc ctc tcg gtg gcg gac ttg atc gtg ggt gcc gtc gtc      418
268 Tyr Ile Val Ser Leu Ser Val Ala Asp Leu Ile Val Gly Ala Val Val
269 65                               70                               75                               80
271 atg cct atg aac atc ctc tac ctg ctc atg tcc aag tgg tca ctg ggc      466
272 Met Pro Met Asn Ile Leu Tyr Leu Leu Met Ser Lys Trp Ser Leu Gly
273                               85                               90                               95
275 cgt cct ctc tgc ctc ttt tgg ctt tcc atg gac tat gtg gcc agc aca      514
276 Arg Pro Leu Cys Leu Phe Trp Leu Ser Met Asp Tyr Val Ala Ser Thr
277                               100                              105                              110
279 gcg tcc att ttc agt gtc ttc atc ctg tgc att gat cgc tac cgc tct      562
280 Ala Ser Ile Phe Ser Val Phe Ile Leu Cys Ile Asp Arg Tyr Arg Ser
281                               115                              120                              125
283 gtc cag cag ccc ctc agg tac ctt aag tat cgt acc aag acc cga gcc      610
284 Val Gln Gln Pro Leu Arg Tyr Leu Lys Tyr Arg Thr Lys Thr Arg Ala
285                               130                              135                              140
287 tcg gcc acc att ctg ggg gcc tgg ttt ctc tct ttt ctg tgg gtt att      658
288 Ser Ala Thr Ile Leu Gly Ala Trp Phe Leu Ser Phe Leu Trp Val Ile
289 145                              150                              155                              160
291 ccc att cta ggc tgg aat cac ttc atg cag cag acc tcg gtg cgc cga      706
292 Pro Ile Leu Gly Trp Asn His Phe Met Gln Gln Thr Ser Val Arg Arg

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293		165		170		175		
295	gag gac aag tgt	gag aca gac ttc tat	gat gtc acc tgg ttc aag gtc	754				
296	Glu Asp Lys Cys	Glu Thr Asp Phe Tyr	Asp Val Thr Trp Phe Lys Val					
297		180		185		190		
299	atg act gcc atc atc aac ttc tac	ctg ccc acc ttg ctc atg ctc tgg	802					
300	Met Thr Ala Ile Ile Asn Phe Tyr	Leu Pro Thr Leu Leu Met Leu Trp						
301		195		200		205		
303	ttc tat gcc aag atc tac aag gcc	gta cga caa cac tgc cag cac cgg	850					
304	Phe Tyr Ala Lys Ile Tyr Lys Ala	Val Arg Gln His Cys Gln His Arg						
305		210		215		220		
307	gag ctc atc aat agg tcc ctc cct	tcc ttc tca gaa att aag ctg agg	898					
308	Glu Leu Ile Asn Arg Ser Leu Pro	Ser Phe Ser Glu Ile Lys Leu Arg						
309	225		230		235		240	
311	cca gag aac ccc aag ggg gat gcc	aag aaa cca ggg aag gag tct ccc	946					
312	Pro Glu Asn Pro Lys Gly Asp Ala	Lys Lys Pro Gly Lys Glu Ser Pro						
313		245		250		255		
315	tgg gag gtt ctg aaa agg aag cca	aaa gat gct ggt ggt gga tct gtc	994					
316	Trp Glu Val Leu Lys Arg Lys Pro	Lys Asp Ala Gly Gly Gly Ser Val						
317		260		265		270		
319	ttg aag tca cca tcc caa acc ccc	aag gag atg aaa tcc cca gtt gtc	1042					
320	Leu Lys Ser Pro Ser Gln Thr Pro	Lys Glu Met Lys Ser Pro Val Val						
321		275		280		285		
323	ttc agc caa gag gat gat aga gaa	gta gac aaa ctc tac tgc ttt cca	1090					
324	Phe Ser Gln Glu Asp Asp Arg Glu	Val Asp Lys Leu Tyr Cys Phe Pro						
325		290		295		300		
327	ctt gat att gtg cac atg cag gct	gcg gca gag ggg agt agc agg gac	1138					
328	Leu Asp Ile Val His Met Gln Ala	Ala Ala Glu Gly Ser Ser Arg Asp						
329	305		310		315		320	
331	tat gta gcc gtc aac cgg agc cat	ggc cag ctc aag aca gat gag cag	1186					
332	Tyr Val Ala Val Asn Arg Ser His	Gly Gln Leu Lys Thr Asp Glu Gln						
333		325		330		335		
335	ggc ctg aac aca cat ggg gcc agc	gag ata tca gag gat cag atg tta	1234					
336	Gly Leu Asn Thr His Gly Ala Ser	Glu Ile Ser Glu Asp Gln Met Leu						
337		340		345		350		
339	ggt gat agc caa tcc ttc tct cga	acg gac tca gat acc acc aca gag	1282					
340	Gly Asp Ser Gln Ser Phe Ser Arg	Thr Asp Ser Asp Thr Thr Thr Glu						
341		355		360		365		
343	aca gca cca ggc aaa ggc aaa ttg	agg agt ggg tct aac aca ggc ctg	1330					
344	Thr Ala Pro Gly Lys Gly Lys Leu	Arg Ser Gly Ser Asn Thr Gly Leu						
345		370		375		380		
347	gat tac atc aag ttt act tgg aag	agg ctc cgc tcg cat tca aga cag	1378					
348	Asp Tyr Ile Lys Phe Thr Trp Lys	Arg Leu Arg Ser His Ser Arg Gln						
349	385		390		395		400	
351	tat gta tct ggg ttg cac atg aac	cgc gaa agg aag gcc gcc aaa cag	1426					
352	Tyr Val Ser Gly Leu His Met Asn	Arg Glu Arg Lys Ala Ala Lys Gln						
353		405		410		415		
355	ttg ggt ttt atc atg gca gcc ttc	atc ctc tgc tgg atc cct tat ttc	1474					
356	Leu Gly Phe Ile Met Ala Ala Phe	Ile Leu Cys Trp Ile Pro Tyr Phe						
357		420		425		430		

**VERIFICATION SUMMARY**

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L:17 M:270 C: Current Application Number differs, Wrong Format

L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date